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20	21	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	40
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140	161	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	240
QY	61	AspTyrHleLeuSerAlaIleGlyIleLeuGlyIleLeuAspTyrHleLeuSerCysHlePheLeuTrp	80
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20	31	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	100
140	301	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	500
QY	101	ThrAlaValIleHleAlaSerLeuValIleValIleAlaSerAlaIleGlyIleLeuGlyIleLeuAspTyrHleLeuSerCysHlePheLeuTrp	120
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QY	141	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	160
140	461	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	540
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140	601	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	600
QY	201	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	220
140	601	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	720
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140	721	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	780
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140	761	AlaSerLeuGlyIleHleLeuPheTrpSerHleLeuSerHleHleHleLeuAlaAla	840
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Sequence 290: Application 05/07/96 295A			
Part No. 05/07/96 295A			
GENERAL INFORMATION:			
APPLICANT: ASKONDAZAVI 21			
APPLICANT: Baker Kevin P.			
APPLICANT: Botsted David			
APPLICANT: Desnoyers June			
Alignment Scores:			
Prod. No.:	5, 040, 149	Length:	1,658
Score:	143,000	Matches:	282
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Identity Match:	100,000	Indels:	0

APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088211
APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-05
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/088217
APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088255
APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-04
APPLICANT: Godowski, Paul J.	PRIOR APPLICATION NUMBER: 60/088734
APPLICANT: Grimaldi, J. Christopher	PRIOR FILING DATE: 1998-06-10
APPLICANT: Garney, Austin L.	PRIOR APPLICATION NUMBER: 60/088738
APPLICANT: Kijavira, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William L.	PRIOR APPLICATION NUMBER: 60/088855
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Semi-conductor and Transistor and Methods	
TITLE OF INVENTION: Acids Encoding the Same	
FILE REFERENCE: P27301056	
CURRENT APPLICATION NUMBER: US/69/989,251A	
CURRENT FILING DATE: 2001-11-20	
PRIOR APPLICATION NUMBER: 60/049787	
PRIOR FILING DATE: 1997-06-16	
PRIOR APPLICATION NUMBER: 60/062250	
PRIOR FILING DATE: 1997-10-17	
PRIOR APPLICATION NUMBER: 60/065186	
PRIOR FILING DATE: 1997-11-12	
PRIOR APPLICATION NUMBER: 60/065311	
PRIOR FILING DATE: 1997-11-13	
PRIOR APPLICATION NUMBER: 60/066776	
PRIOR FILING DATE: 1997-11-24	
PRIOR APPLICATION NUMBER: 60/075945	
PRIOR FILING DATE: 1998-03-25	
PRIOR APPLICATION NUMBER: 60/078910	
PRIOR FILING DATE: 1998-03-26	
PRIOR APPLICATION NUMBER: 60/083322	
PRIOR FILING DATE: 1998-04-28	
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PRIOR FILING DATE: 1998-06-24	
PRIOR APPLICATION NUMBER: 60/090435	
PRIOR FILING DATE: 1998-06-24	
PRIOR APPLICATION NUMBER: 60/090444	
PRIOR FILING DATE: 1998-06-25	

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 121 GACCAATTCACATCATCTGGCTTGGTATTTCAGGAGAGACATCCATCCATCATCAT 189
Q7 41 ThrValAlaSerAlaGlyAsnIleGlyLeuAspGlyIleLeuSerGlyThrIleGlyPhe 60
Db 181 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249
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RESULT 6

US-09 989-722-290

Sequence 200, Applicant: US/00569722

Patent No. 9820020072067A1

GENERAL INFORMATION:
APPLICANT: Applicant, J. J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fink, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Griffiths, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurley, Austin L.
APPLICANT: Kijavits, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pech, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watkiss, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William L.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: A1838 Receding the Same
FILE REFERENCE: P27301063
CURRENT APPLICATION NUMBER: US/09/999,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/045797
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fonq, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kligwin, Ivar J.
APPLICANT: Nardier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Rarclain
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 15730, 1373
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-03
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435

1	APPLICANT: Williams, P. Mickey	2	PRIOR FILING DATE: 1998-06-10
2	APPLICANT: Wood, William I.	3	PRIOR APPLICATION NUMBER: 60/088855
3	APPLICANT: Zhang, Zemin	4	PRIOR FILING DATE: 1998-06-11
4	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	5	PRIOR APPLICATION NUMBER: 60/088855
5	FILE OF INVENTION: Acids Encoding the Same	6	PRIOR FILING DATE: 1998-06-11
6	FILE REFERENCE: P2730P1C57	7	PRIOR APPLICATION NUMBER: 60/088855
7	CURRENT APPLICATION NUMBER: 08-09-009, 009, 009, 009	8	PRIOR FILING DATE: 1998-06-11
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Alignment Scores:

Pred. No.:	5,04e-169	Length:	1658
Score:	1431.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

[illegible]

Sun Dec 15 08:43:55 2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1443)
Strausborg, R.
Direct Submission
Submitted (13 JUN 2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
MGC project url: <http://mgc.nhl.nih.gov>
Contact: MGC help desk
Email: mgc-help@mail.nih.gov
Tissue Procurement: Marcelo Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Hosack, Yaron Butterfield,
Susanna Chan, Roadman Chiu, Chris Fjell, Erin Garland, Ran Guha,
Leticia Hsiao, Martin Kizyewski, Peter Kutscher, Oliver Lee, Sue
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandey, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schell, Thorne Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Marjanda Tsai, Betasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium (<http://imgc.nhl.nih.gov>)
Series: IRAC plate: 67 Row: 1 Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: hexamer frequency ORF
analysis, Similarity but not identity to protein.

Location/Qualifiers
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/class="type="uterus, pregnant mouse"
/clone_lib="Soares_NMPu"
/lab_host="DH10B"
/note="Vector: pMT730-Pac"
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VFQAVVGNASLKLKPLVGLAALVLYPLFSEFSGNARLTKTGATSELEIVLYN
ASSSLRLAPRWFQPLVAVASQVLCARISEVSESEDI NSDRVTRFVSVLYNLT
INRTYSECHENLAEATGSEIRVISEVFFPFLQLINSGSPFVSSSAFVAGWALLSL
SCCLMLR"

BASE COUNT 486 a 330 c 314 g 313 t
ORIGIN

Alignment Scores:
Pred. No.: 7,8e-110 Length: 1343
Score: 1253.50 Matches: 217
Percent Similarity: 92.23% Conservat: 14
Best Local Similarity: 87.44% Mismatches: 21
Query Match: 87.60% Indels: 1
Gaps: 1

US-09-915-789A-5 (1-282) x BC032925 (1-1343)

QY 1 MetAlaSerLeuGlyGlnIleLeuPheTrpSerIleIleSerIleIleIleIleIleAla 20
DB 51 ATGGCTTCCTTGGGCGAGATCATCTTTCGAGTATATTAAGATCATCATCATCGCT 110
QY 41 GlyAlaIleValLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 40
DB 111 GGCGGCAATCGACATCATCTTGGCTTGGCATTCAGGAAAGCATTCAAGGCTCAAG 170

US-09-915-789A-5 (1-282) x AK026071 (1-1811)

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DB 71 ATGGCTTCCTTGGGCGAGATCATCTTTCGAGTATATTAAGATCATCATCATCGCT 130
QY 21 GlyAlaIleValLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 40
DB 131 GGAGCAATTCGACATCATCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 170
QY 41 ThrValAlaSerAlaGlyGlnIleLeuPheTrpSerIleIleSerIleIleIleIleIle 60
DB 191 ACTGTGCGGCTCAGTGGGAAATTCGGGAGATGGAATGGAATGGAATGGAATGGAAT 250
QY 61 AspIleIleLeuSerAspIleValIleIleIleIleIleIleIleIleIleIleIleIle 80
DB 251 GAGATCAAACTTCTGATATCGTATACAAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 310
QY 81 HisGluPheLeuGlyGlnIleLeuPheTrpSerIleIleSerIleIleIleIleIleIle 100
DB 311 CATGAGTCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 370
QY 101 ThrAlaValPheAlaAspIleValIleValIleValIleValIleValIleValIleVal 120
DB 371 ACAGCAGTGTCTGATATCAATGATAGTGGCAATGCGCTCTTGGAGCTTGAAGGCTG 430
QY 121 GluLeuThrAlaAlaGlyGlnIleLeuPheTrpSerIleIleSerIleIleIleIleIle 140
DB 431 CAATTCACATGCTGGGCTTCAAAATGTTATATATATATATATATATATATATATATAT 490
QY 141 AlaAspLeuGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 160
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QY 161 AlaSerSerGluThrLeuAlaGlyGlnIleLeuPheTrpSerIleIleIleIleIleIle 180
DB 551 GCGAGTTCAGAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610
QY 181 TrpAlaSerGluValAspGlnGlyAlaAspPheSerGluValSerAspThrSerPheGlu 200
DB 611 TGGGCATCCCAAGTGTGATCAGGAGGCAAGCTCTCGGAAGTCTCCAAATACAGGCTT 670
QY 201 LeuAspSerGluAspValThrMetIleValValSerValIleValIleValIleVal 220
DB 671 CTGAGCTCTCGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
QY 221 AsnIleIleSerGlySerIleIleIleIleIleIleIleIleIleIleIleIleIleIle 240
DB 731 AACCATATCTCTATGATTGAAATGCAATTCGCAAGGCAAGGCAAGGCAATCAAAAGT 790
QY 241 ThrGluSerGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 260
DB 791 ACAGAACTGGAGATCAAAAGGCGGAGTACACCAATACCTTCAAGGCTTCAAGGCTT 850
QY 261 CysValSerSerPhePheAlaIleSerTrpAlaLeuLeuProIleSerTrpIleLeuMet 280
DB 851 TGTGTCCTCTCTTCTTGGCATCAGCTGGGCACTTGGGCACTTGGGCACTTGGGCACT 910
QY 281 LeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 300
DB 911 CTAAAA 916

RESULT 12
BC032925
LOCUS BC032925 1343 bp mRNA linear R5D 13-JUN-2002
DEFINITION Mus musculus. Similar to hypothetical protein FLJ22418, clone

ACCESSION BC032925
VERSION BC032925.1 GI:21410734

KEYWORDS MGC,
house mouse,
Mus musculus

ORGANISM



FH Key Location/Qualifiers
FI 1,049
FI Zoned "Human B7-H4 protein"
FI /Product

FN W0200210187 AL
FA 07-FEB-2002

XX 26-JUL-2001 2001W0281440
XX 27-JUL-2000 2000W022991P

XX 05-SEP-2000 2000W0281440
XX 06-SEP-2000 2000W0281440

XX 07-SEP-2000 2000W0281440
XX 08-SEP-2000 2000W0281440

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FH Key Location/Qualifiers
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FH Key Location/Qualifiers
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FI Zoned "Human B7-H4 protein"
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XX 31-SEP-2000 2000W0281440
XX 01-OCT-2000 2000W0281440

us-09-915-789a-5.rni

Sun Dec.15 08:43:59 2002

ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: 90-IBM/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 99/08/702,525
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 05/09/205,697
FILING DATE: 03-Mar-1994
ALTERNATE/ASHT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BW1-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 99...1025
US-08-702-525-20

Alignment Scores:
Prod. No.: 5,77e-10 Length: 1151
Score: 157.50 Matches: 60
Percent Similarity: 45.56% Conservative: 60
Best Local Similarity: 22.99% Mismatches: 99
Query Match: 11.01% Indels: 42
DB: 4 Gaps: 11

US-09-915 789A 5 (1 282) x US-08-702-525-20 (1-1151)
QY 37 TlethrValThrThrValAlaSerAlaGlyAsnIle-----GlyIle 50
Db 141 GTGACAGCTCTGCTCATCTCATCTGTTTCGGTGGAGCAGCAGCTTATTTCAATGG 200
QY 51 AspGlyIleLeuSerCysIlePhe-----GluProAspIleLysLeuSerAspIleVal 68
Db 201 ACTGCATATCTGCGTGGCCATTATCAAAAGGCTCAAAACATAGCTGAGTGGTGGTGA 260
QY 69 TleGlnIlePheLysGlyValLeuGlyLeuValHisGlyPheLysGlyLysAsp 88
Db 261 GIATTTTGGCAGCAGCAGCAAAAGTGG-----GTTCGTAGCAGCAGCTATTTGGCAGAG 417
QY 89 GluLeuSerGluGlnAspGluMetPheArgGlyArgThrAlaValPheAlaAspIleVal 108
Db 318 AAACCTTCATAGTGTGAATGCCAGTACCTGGGGCCGACAGAGCTT-----GACAGG--- 468
QY 105 TleValGlyAsnAlaSerLeuArgLeuLysAsnValGlnLeuThrAspAlaIleThrIle 128
Db 423 GATTGTTTATAIA/AAAAAAGGCGACGAGATCAATATACCTCCACAGCATATAACA 482
QY 369 -----AAAGAGTGGAGTGAACACTTCCAAATGTCATCAAGAGCAATGCTGAT 422
QY 129 GysGlyIleIleIleIleSerGlyLysGlyAsnAlaAsnValLeuLys----- 146
Db 423 GATTGTTTATAIA/AAAAAAGGCGACGAGATCAATATACCTCCACAGCATATAACA 482
QY 147 -----ThrGlyAlaPheSerMetProGlyValAsnValAspIleAsnAlaSer 162
Db 483 GAAATGTCAGTGAATGCAACTTCAGTGAACCTGAAATAAACCTGGCTTCACATGTAACA 542
QY 163 SerGluThr-----LeuArgCysGluAlaProArgTrpPheProGlnProThrVal 179
Db 543 GGAATTCGGCATAAATTCACCTGACCTCTAAGCAAGGTGACGGGAACCTAAGAG 602
QY 180 ValTrpAlaSerGlnValAspGlnGlyAlaAsnPheSerGluValSerAsnThrSerPhe 199
Db 603 ATGATTTTCGATACATAATCAACATATACATCATATGAT-----AACATG 650
QY 200 GluLeuAsnGlnAsnValThrMetLysValValSerValLeuThrValThrIle 219
Db 651 CAGATATACAGAAATATGTCACA---GAAGTCTTCATATCTCCAGCAGCGCTCTCT 707
QY 220 -----AsnAsuThrTyrSerCysMetIleGluAsnAspIleAla 232
Db 708 TCATTCGGGATGTGTGTGCATATGACGCTCTCTGTGTCTGCGAAACGAGTCAATG 767
QY 233 LysAlaThrGlyAspIleLysValThr-----GluSerGluIleLeu 246
Db 768 AAGATTTCTCCAAACCTCTCAATTTCTCACTCAACAGCTTCCATCTCTCAACAGCTATTCG 827
QY 246 sArgArgSerHisLeuGluLeuLeuAsnSerLysAlaSerLysValSerPhePhe 266
Db 828 AAGGAGATTACAGCTTCAGTACTGTGGCCCTCTCTCTCTGATGCTGCTATCATTTGA 887
QY 266 e 266
Db 888 T 888

RESULT 15

US-08-702-525-20
Sequence 20, Application US/08702525
Patent No. 6,291,660

GENERAL INFORMATION:

APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopolo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6,291,660e1 Forms of T Cell Costimulatory
TITLE OF INVENTION: Molecules and Uses Thereof
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & CYCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

GenCore version 5.1.3
Copyright (c) 1992 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 18:48:39 : Search time 2206 Seconds

(without alignments)

2070 221 hits for cell of 140,500

Title: US-09-915-789A-5

Perfect score: 1431

Sequence: 1 MASLGLQIFWLSISIIIIILA.....SSPFAISWALLPSPFYILK 282

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Chcd: 16154066 seqs, 8097743376 residues

Total number of hits satisfying check parameters: 22068132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-GSS=0.02 -GSS1=0.01 -GSS2=0.01 -GSS3=0.01 -GSS4=0.01 -GSS5=0.01 -GSS6=0.01 -GSS7=0.01 -GSS8=0.01 -GSS9=0.01 -GSS10=0.01
-DB-EST-QPMT=rascap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STAP=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=Trans40 -cdi -LIST 15
-DOALIGN=200 -THP_SCORE=pct -THP_MAX=100 -THP_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=fto -NUPM=ext -HEAFSLZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09-915789A -GCGN_1_1_1716 -grunat_09122002_152022_12998 -MCS3_6 -ICSD=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LANGLOC -PFW_TIMEOUT=120
-WAPN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6 -FCAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
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8: em_hic: *
9: qb_est1: *
10: qb_est2: *
11: qb_hic: *
12: qb_est3: *
13: qb_est4: *
14: qb_est5: *
15: em_estin: *
16: em_estom: *
17: qb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
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21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	993	75.4	751	13	B1454643
2	993	69.4	751	13	B1454643
3	837	58.5	670	10	B666051
4	832	58.2	917	10	B6573890
5	738.5	52.6	639	10	B6381863
6	750.5	52.4	845	12	B6680206
7	637	44.5	658	10	B6308473
8	621	43.4	487	9	A1155439
9	499	24.2	432	9	A1793522
10	483	33.8	888	14	BQ734734
11	476	33.3	840	12	BQ172919
12	470	32.8	436	17	AQ479841
13	419	29.3	693	13	B1043488
14	395.5	27.6	916	14	BQ731562
15	390.5	27.3	914	14	BQ734151
16	387	27.0	679	13	BQ071648
17	385	26.9	292	9	AA333549
18	350.5	24.5	619	9	AL070863
19	283	19.8	686	10	B6551556
20	260.5	18.2	660	13	B6488658
21	259	18.1	260	9	AA117088
22	249	17.3	653	13	B6498157
23	247.5	17.3	675	13	B6492723
24	234.5	16.4	750	12	BQ574312
25	232	16.2	1003	4	A0330047
26	229.5	15.6	857	3	AL537641
27	221.5	15.5	919	5	AL545252
28	215	15.0	471	17	CNS046AY
29	211	14.7	863	14	BQ293277
30	207.5	14.7	541	12	BQ310335
31	206.5	14.4	649	14	BQ711172
32	205.5	14.4	629	10	BQ620731
33	205	14.4	629	12	BQ710433
34	205	14.3	614	13	B6487661
35	201.5	14.1	899	14	BQ706029
36	199.5	13.9	713	12	BQ390011
37	197.5	13.8	1074	14	BQ278722
38	197	13.8	473	10	BQ477170
39	195	13.6	498	12	B1221059
40	194	13.6	1053	13	B1766909
41	191	13.3	924	12	B1528953
42	189.5	13.2	1079	17	CNS0514G
43	189	13.2	478	10	BQ275413
44	188.5	13.2	818	12	BQ38725
45	188	13.1	872	13	B1518879

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LOCUS	B1454643	mRNA sequence			
DEFINITION	B1454643.1	GI:15245299			
ACCESSION	B1454643				
VERSION	B1454643.1				
KEYWORDS	EST				
SOURCE	house mouse				
ORGANISM	Mus musculus				
REFERENCE	1	(bases 1 to 757)			
AUTHORS	EMBL				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				


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Db 670 AA-AACACATAGTGTATGATTGAAACAGGACTTGGGAAAGCCAGCGGGA-----CCTCA- 724
QY 240 ValThrGluSerGluIleLysArgArgSerHisLeuGlnLeuLeuAsnSerLysAlaSer 259
Db 725 GTGGCGGATTCGGCGTCAACAGCGAGTCCAGG----- 757
QY 250 LeuCysValSerSerPhePheAlaIleSerTrpAla 271
Db 758 --TCATTGGG-----AACCGGGC 775

RESULT 5
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LOCUS 601272421p1 MCL_CGAF_Mam1 Mus musculus cDNA clone IMAGE:601637 5',
DEFINITION mRNA sequence.
ACCESSION BE381883
VERSION BE381883.1 GI:9327248
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 639)
AUTHORS NIH MCC http://www.ncbi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: coapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1AM8787 row: j column: 66
High quality sequence stop: 591.
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            /clone="IMAGE:3601637"
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            /lab_host="DH10B"
            /note="organ: mammary; Vector: pCMV-SVcat9, Site1, Site2,
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            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
BASE COUNT 171 a 169 c 158 g 141 t
ORIGIN

Alignment Scores:
pred No.: 7,2e-91 Length: 639
Score: 798.50 Matches: 159
Percent Similarity: 92.43% Conservative: 12
Best Local Similarity: 85.95% Mismatches: 14
Query Match: 55.80% Indels: 2
DB: 10 Gaps: 1

US-09-915-789A-5 (1-282) x BE381883 (1-639)

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Db 60 ATGGCTTCCTTGGGCGAGATCATCTTTTGGAGIATTATTAATCATCATCATCTGCT 119
QY 21 CysAlaIleAlaGluIleIleGluPheGluTrpSerGluCysIleIleValIle 40
Db 120 CGGCCCAACGACATCATCATCTGCTTTGGAGATTTCAGAGAGACATCATCATGCG 179
QY 41 ThrValAlaSerAlaGlyAsnIleGlyGluAspGlyIleLeuGluCysThrPheGlu 60

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Db 180 ACCCTCACCTCAGCTCGAAACATTCGAGAGGACGGAGACCTCGAGCTGAC-ITTCAGAACT 248
QY 61 AspIleLysLeuSerAspIleValIleIleGlnTrpLeuLysGluGlyValLeuThrLeuVal 40
Db 239 GACATCAAACTCAACGGCATCTGTCATCCAGTGGCTGAAAGAGAGGATCAAAATCTTGGG 248
QY 91 HisGluPheLysGluGlyLysAspGlnLeuSerGluGluAspGluMetPheAspGlyAla 100
Db 299 CACGAGTTCAAAGAAAGCAAGAGAGGAGCTCTCACAGACACATGATGTCAGAGAGAG 478
QY 101 ThrAlaValPheAlaAspGlnValIleValIleValIleValIleValIleValIleVal 120
Db 359 ACAGCAGCTGTTGTCATGATCAGGTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 418
QY 121 GlnLeuPheAspAlaGlyThrTrpLysCysTrpIleIleThrSerLysSerLysSerLys 140
Db 419 CAGTCAAGGATCTGGACATCTACATGCTTACATCGGACCTGCAAAAGAGAGAGAGAG 478
QY 141 AlaAsnLeuIleTrpLysThrGlyAlaPheSerMetPheGluValValAsnValAspTyr 160
Db 479 GCAAACTTCAGTATAACACCGAGAGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 548
QY 539 GCGAGTTCAGAGAGATTTACGCTGAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 595
Db 181 TrpAlaSerGlnVal 185
Db 596 TGGGCTATCGAGTGG 610

RESULT 6
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LOCUS 602514531t1 M.H.ME1_2 Homo sapiens cDNA clone IMAGE:425775 5',
DEFINITION mRNA sequence.
ACCESSION BE680206
VERSION BE680206
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH WGS http://www.ncbi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: coapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1CM1147 row: d column: 16
High quality sequence stop: 657.
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    Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="M.H.ME1_2"
            /clone_lib="NIH_MGC_83"
            /lab_host="DH10B (11 phage-resistant)"
            /note="organ: testis; Vector: pBluescript II (GibcoBRL)
            Site1: SfiI (accgcttaagc); Site2: SfiI (accattatgac)
            ) ; 5' and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-CAGCGCATTAATGGC-3' and 3' adaptor
            sequence: 5'-ATTTCATAGAGCGGCGGACATC-4' (40)BN 3'
            (where B = A, C, G and N = A, C, G, or T). Average
            insert size 1.4 kb (range 0.5-4.9 kb). 11/15 colonies
            contained inserts by PCR. This library was enriched for

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ACCESSION BG172919
VERSION BG172919.1 GI:12679609
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuDen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 15:33:48 / Search time 3107 seconds
(without alignments)
7952.456 Million cell updates/sec

Title: US-09-915-789A-6
Perfect score: 849
Sequence: 1 atggttcctgggcacat.....cttaactgaatgtaataaa 849

Scoring table: IDENTITY_NUC
Gapop 10 0 / Gapext 1.0

Searched: 2054640 seqs, 14551402873 residues
number of hits satisfying chosen parameters: 410280

Minimum DP seq length: 0
Maximum DP seq length: 205030500

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:
2: gb_hu:
3: gb_in:
4: gb_cm:
5: gb_or:
6: gb_pt:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gl_si:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hu:
18: em_in:
19: em_ma:
20: em_um:
21: em_or:
22: em_or:
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25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vi:
30: em_htg_hu:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pan:
35: em_htg_ror:
36: em_htg_mam:
37: em_htg_vrl:
38: em_sy:
39: em_htgo_hu:
40: em_htgo_mus:
41: em_htgo_other:

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	% Query Match	Length	DB	ID	Description
1	849	100.0	1065	6	AX375858	Sequence
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3	849	100.0	1658	6	AX376150	Sequence
4	849	100.0	1658	6	AX395215	Sequence
5	849	100.0	1658	6	AX403403	Sequence
6	849	100.0	1658	6	AX468680	Sequence
7	849	100.0	2603	6	AX403048	Sequence
8	849	100.0	2626	6	AX375858	Sequence
9	849	100.0	2627	6	AX156350	Sequence
10	849	100.0	2627	6	AX366624	Sequence
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12	737.8	86.9	44564	9	HS11035A1	Sequence
13	631.2	74.3	1343	10	BC032925	Sequence
14	422.9	49.7	456	6	AX182037	Sequence
15	358.8	42.3	171595	9	AX490051	Sequence
16	344.4	40.4	336	6	AX098101	Sequence
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30	257.8	30.4	153215	2	AC110845	Sequence
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33	257.8	30.4	153215	2	AC110845	Sequence
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37	257.8	30.4	153215	2	AC110845	Sequence
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40	257.8	30.4	153215	2	AC110845	Sequence
41	257.8	30.4	153215	2	AC110845	Sequence
42	257.8	30.4	153215	2	AC110845	Sequence
43	257.8	30.4	153215	2	AC110845	Sequence
44	257.8	30.4	153215	2	AC110845	Sequence
45	257.8	30.4	153215	2	AC110845	Sequence

ALIGNMENTS

Result No	Score	% Query Match	Length	DB	ID	Description
1	849	100.0	1065	6	AX375858	Sequence
2	849	100.0	1658	6	AX092329	Sequence
3	849	100.0	1658	6	AX376150	Sequence
4	849	100.0	1658	6	AX395215	Sequence
5	849	100.0	1658	6	AX403403	Sequence
6	849	100.0	1658	6	AX468680	Sequence
7	849	100.0	2603	6	AX403048	Sequence
8	849	100.0	2626	6	AX375858	Sequence
9	849	100.0	2627	6	AX156350	Sequence
10	849	100.0	2627	6	AX366624	Sequence
11	847.4	99.8	1811	9	AK026071	Sequence
12	737.8	86.9	44564	9	HS11035A1	Sequence
13	631.2	74.3	1343	10	BC032925	Sequence
14	422.9	49.7	456	6	AX182037	Sequence
15	358.8	42.3	171595	9	AX490051	Sequence
16	344.4	40.4	336	6	AX098101	Sequence
17	259.6	30.6	199673	10	AL669872	Sequence
18	257.8	30.4	153215	2	AC110845	Sequence
19	257.8	30.4	153215	2	AC110845	Sequence
20	257.8	30.4	153215	2	AC110845	Sequence
21	257.8	30.4	153215	2	AC110845	Sequence
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23	257.8	30.4	153215	2	AC110845	Sequence
24	257.8	30.4	153215	2	AC110845	Sequence
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 Baker, K.P.; Chen, J.; Desnovers, L.; Goddard, A.; Godowski, P.J.;
 Gurney, A.L.; Pan, J.; Smith, V.; Watanabe, C.K.; Wood, W.I. and
 Zhuang, Z.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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 JOURNAL Patent: WO 0168848-A 217 20-SEP-2001;
 Genentech, Inc. (US)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 Goddard, A.; Godowski, P.J.; Gurney, A.L.; Hillan, K.L.; Polakis, P.;
 Smith, V.; Wood, W.I.; Wu, T.D. and Zhang, Z.
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 Genentech, Inc. (US)
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FEATURES CORLIXA CORPORATION (US)

SOURCE Location/Qualifiers

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AX366624 /db_xref="taxon:6065"

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AX366624

DEFINITION

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VERSION

AX366624.1 GI:18698046

KEYWORDS

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CORLIXA

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ARTBRS

TITLE

JOURNAL

FEATURES

SOURCE

Location/Qualifiers

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QY 61 GAGCAATTCGACATCATCTGGCTTTGGTATTTGAGGAGACATCTCATCAAGACCT 120

Db 143 GAGCAATTCGACATCATCTGGCTTTGGTATTTGAGGAGACATCTCATCAAGACCT 202

QY 121 ACTGTGGCTCAGCTGGGACATTTGGGAGCATCTGATCTGATCTGATCTGATCTG 180

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 i (Lanes 1 to 4464)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (20-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clinerequest@sanger.ac.uk
 On Dec 22, 1994 this sequence version replaced 415591194.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission, corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu), where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases. EM, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
<http://www.sanger.ac.uk/ftp/pepdb/pepdb.html>
 from the library P0015 constructed at the Wellcome Park Cancer Institute by the group of Pictet de Jong. For further details see
<http://barpac.med.buffalo.edu/>
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 IMPORTANT: This sequence is not the entire insert of clone RP5 1025A1. It may be shorter because we only sequence overlapping sections only, or longer because we arrange for a small overlap between neighbouring submissions.
 The true left end of clone RP4-799p15 is at 94555 in this sequence. The true right end of clone RP4-508C11 is at 104 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/ftp/ch20/>

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11

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 RESULT 4
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 Sequence: 290; Application: 03/09/98/290A
 Patent No.: US20020177164A1
 GENERAL INFORMATION:
 APPLICANT: Aaker, J. Aaker, J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Barstow, David
 APPLICANT: Besmeyer, John
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 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gottschon, Mary E.
 APPLICANT: Gaddard, Arthur J.
 APPLICANT: Gadowski, Paul J.
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Asst. In L.
 APPLICANT: Kipfer, Ivan J.
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 APPLICANT: Pan, James
 APPLICANT: Pomeroy, Nicholas F.
 APPLICANT: Ray, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Thomas, Ianley
 APPLICANT: Watanabe, Chieko K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William L.
 APPLICANT: Zeman, Zeman
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: As Also Enumerated the Same
 FILE REFERENCE: 127-001066
 CURRENT FILING DATE: 2001-11-29
 PRIOR FILING DATE: 1997-06-16
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1 APPLICANT: Kijavie, Ivan J.
2 APPLICANT: Kapier, Mary A.
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9 APPLICANT: Williams, P. Mickey
10 APPLICANT: Wood, William L.
11 APPLICANT: Zhang, Zemin
12 TITLE OF INVENTION: Secreted and Transformed Polypeptide and Peptide
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Query Match: 100.0%; Score 849; DB 10; Length 1658;

Best Local Similarity 100.0%; Pred. No. 6,11c 266;

Matches 849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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53 PRIOR APPLICATION NUMBER: 60/090557
54 PRIOR FILING DATE: 1998-06-24
55 PRIOR APPLICATION NUMBER: 60/090676
56 PRIOR FILING DATE: 1998-06-25
57 PRIOR APPLICATION NUMBER: 60/090678
58 PRIOR FILING DATE: 1998-06-25
59 PRIOR APPLICATION NUMBER: 60/090690
60 PRIOR FILING DATE: 1998-06-25
61 PRIOR APPLICATION NUMBER: 60/090694
62 PRIOR FILING DATE: 1998-06-25
63 PRIOR APPLICATION NUMBER: 60/090695
64 PRIOR FILING DATE: 1998-06-25
65 PRIOR APPLICATION NUMBER: 60/090696
66 PRIOR FILING DATE: 1998-06-25
67 PRIOR APPLICATION NUMBER: 60/090662
68 PRIOR FILING DATE: 1998-06-26
69 PRIOR APPLICATION NUMBER: 60/090663
70 PRIOR FILING DATE: 1998-06-26
71 PRIOR APPLICATION NUMBER: 60/091360
72 PRIOR FILING DATE: 1998-07-01
73 PRIOR APPLICATION NUMBER: 60/091478

1 PRIOR APPLICATION NUMBER: 60/091544
2 PRIOR FILING DATE: 1998-07-01
3 PRIOR APPLICATION NUMBER: 60/091519
4 PRIOR FILING DATE: 1998-07-02
5 PRIOR APPLICATION NUMBER: 60/091626
6 PRIOR FILING DATE: 1998-07-22
7 PRIOR APPLICATION NUMBER: 60/091633
8 PRIOR FILING DATE: 1998-07-22
9 PRIOR APPLICATION NUMBER: 60/091978
10 PRIOR FILING DATE: 1998-07-07
11 PRIOR APPLICATION NUMBER: 60/091982
12 PRIOR FILING DATE: 1998-07-07
13 PRIOR APPLICATION NUMBER: 60/092182
14 PRIOR FILING DATE: 1998-07-09
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Query Match 180.0%; Score 84%; 18 10; Length 1658;
Best local Similarity 100.0%; Pred. No. 6, 1e-266;
Matches 919; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1	PRIOR APPLICATION NUMBER:	60709054
2	PRIOR FILING DATE:	1998-08-24
3	PRIOR APPLICATION NUMBER:	607090542
4	PRIOR FILING DATE:	1998-08-24
5	PRIOR APPLICATION NUMBER:	607090557
6	PRIOR FILING DATE:	1998-08-24
7	PRIOR APPLICATION NUMBER:	607090676
8	PRIOR FILING DATE:	1998-06-25
9	PRIOR APPLICATION NUMBER:	607090678
10	PRIOR FILING DATE:	1998-08-25
11	PRIOR APPLICATION NUMBER:	607090696
12	PRIOR FILING DATE:	1998-08-25
13	PRIOR APPLICATION NUMBER:	607090694
14	PRIOR FILING DATE:	1998-08-25
15	PRIOR APPLICATION NUMBER:	607090695
16	PRIOR FILING DATE:	1998-08-25
17	PRIOR APPLICATION NUMBER:	607090706
18	PRIOR FILING DATE:	1998-08-25
19	PRIOR APPLICATION NUMBER:	607090892
20	PRIOR FILING DATE:	1998-08-26
21	PRIOR APPLICATION NUMBER:	607090894
22	PRIOR FILING DATE:	1998-08-26
23	PRIOR APPLICATION NUMBER:	607090900
24	PRIOR FILING DATE:	1998-07-01
25	PRIOR APPLICATION NUMBER:	6070909478
26	PRIOR FILING DATE:	1998-07-02
27	PRIOR APPLICATION NUMBER:	607090944
28	PRIOR FILING DATE:	1998-07-01
29	PRIOR APPLICATION NUMBER:	607090949
30	PRIOR FILING DATE:	1998-07-02
31	PRIOR APPLICATION NUMBER:	6070909643
32	PRIOR FILING DATE:	1998-07-02
33	PRIOR APPLICATION NUMBER:	607090978
34	PRIOR FILING DATE:	1998-07-03
35	PRIOR APPLICATION NUMBER:	607090992
36	PRIOR FILING DATE:	1998-07-07
37	PRIOR APPLICATION NUMBER:	607090992
38	PRIOR FILING DATE:	1998-07-07

Query Match: 100.0%; Score: 849; DB: 10; Length: 1658;

Category	Count	Percentage
Exact Match	100	100.0%
Best Local Similarity	100	100.0%
Matches	849	84.9%
Mismatches	0	0.0%
Labels	0	0.0%
Gaps	0	0.0%

1	ATGGCTTCGCTGGAGGAAAGACGCTTCTTCGGAGTAAATATGACATCAATATATATCTGGCT	40
61	ATGGCTTCGCTGGAGGAAAGACGCTTCTTCGGAGTAAATATGACATCAATATATATCTGGCT	120
61	GGACCAATTCGACGTCATCATTCGGCTTTTATATATTCAGAGGAGCACTGCAATCACTATCAAT	120
121	GGACCAATTCGACGTCATCATTCGGCTTTTATATATTCAGAGGAGCACTGCAATCACTATCAAT	160
121	ACTGTGCTTCAGCTGGCAACATTCGGAGAGCAAGAAATCTTGAGTGCACCTTTTGAAGCT	180
181	ACTGTGCTTCAGCTGGCAACATTCGGAGAGCAAGAAATCTTGAGTGCACCTTTTGAAGCT	240
181	GACATCAAACTTCTTGATATGCTATATCAATGCTTCAGACCAAGCTGCTTTAGCTCTGCTGCT	240
241	GACATCAAACTTCTTGATATGCTATATCAATGCTTCAGACCAAGCTGCTTTAGCTCTGCTGCT	300
241	CATGAGTCTCAAAAGAAAGAAAGCAAGTGGTGGAGGAGAGATCAAAATGTCATCAAGAGCTGG	300
401	CATGAGTCTCAAAAGAAAGAAAGCAAGTGGTGGAGGAGAGATCAAAATGTCATCAAGAGCTGG	460
401	AACATCACTCTCTCTTATCAAAATCAATATATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	460
461	AACATCACTCTCTCTTATCAAAATCAATATATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	460
461	CAATCAACATGCTGGGACGTCACAAATCTTATATATGATCTTTTAAATCAAGAGAGCAAT	120
461	CAATCAACATGCTGGGACGTCACAAATCTTATATATGATCTTTTAAATCAAGAGAGCAAT	460

*
PRIOR APPLICATION NUMBER: 60/091178
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091644
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092132
PRIOR FILING DATE: 1998-07-09

Query Match: 100.0%; Score 849; DB 10; Length 1658;

Best Local Similarity 100.0%; Pred. No. 6, 1e-266;

Matches 849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTTCCTGGGCGAGATCTCTCTGGCAATATAATAGATATCATCATTAATCTGGCT	60
Db	61	ATGCTTCCTGGGCGAGATCTCTCTGGCAATATAATAGATATCATCATTAATCTGGCT	120
QY	61	GAATCAATTCGATTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	120
Db	121	GAATCAATTCGATTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	180
QY	121	ACTGTCGCTTCAGCTGGAGCAATTCGGAGAGCAATTCGGAGAGCAATTCGGAGAGCA	180
Db	181	ACTGTCGCTTCAGCTGGAGCAATTCGGAGAGCAATTCGGAGAGCAATTCGGAGAGCA	240
QY	181	GATATCAAACTTCTCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT	240
Db	241	GATATCAAACTTCTCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT	300
QY	241	CATGAGTTCAAAAGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT	300
Db	301	CATGAGTTCAAAAGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT	360
QY	301	AACATCATGTTCTCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT	360
Db	361	AACATCATGTTCTCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT	420
QY	361	CAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
Db	421	CAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	480
QY	421	GTTAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480
Db	481	GTTAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540
QY	481	GTTAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540
Db	541	GTTAAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600
QY	541	TGGCATGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
Db	601	TGGCATGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	660
QY	601	CTCAACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
Db	661	CTCAACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
QY	661	AATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	720
Db	721	AATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	780
QY	721	ACAAATGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	780
Db	781	ACAAATGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	840

QY	781	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	840
Db	841	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	900
QY	841	CTAAATAAA 849	
Db	901	CTAAATAAA 909	

Search completed: December 12, 2002, 16:54:12
Job time: 105 secs



Genfore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 14:06:03 : Search time 2210 seconds
(without alignments)
6221.705 Million cell updates/sec

Title: US-09-915-789A-6

Perfect score: 849

Sequence: 1 atpctctctgagcgaat.....cttactatctactaaat aa 849

Scoring table: IDENTITY_NOC

Gapop 10.0, Gapop 1.0

Searched: 16154066 seqs, 8017743376 residues

1 number of hits satisfying chosen parameters: 1210312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba: *

2: em_esthum: *

3: em_estin: *

4: em_estma: *

5: em_estov: *

6: em_estpl: *

7: em_estro: *

8: em_hic: *

9: qb_est1: *

10: qb_est2: *

11: qb_hic: *

12: qb_est3: *

13: qb_est4: *

14: qb_est5: *

15: em_estfun: *

16: em_estom: *

17: qb_oss: *

18: em_oss_hum: *

19: em_oss_inv: *

20: em_oss_pln: *

21: em_oss_vrt: *

22: em_oss_fun: *

23: em_oss_mean: *

24: em_oss_mus: *

25: em_oss_other: *

26: em_oss_pro: *

27: em_oss_rnd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	588	69.3	751	14	BM981657 GI 101181
2	522.4	62.7	757	13	U1454643
3	414.6	48.8	670	10	BM666051
4	413.2	48.7	917	10	BM573890
5	389.6	45.9	845	12	BM480206
6	380.8	44.9	639	10	BM481884

7	344.6	37.1	487	9	AI155439
8	288	31.1	443	9	AI179522
9	286	31.9	436	17	AQ479631
10	286.6	34.0	658	10	BE308474
11	246	27.8	292	9	AA333519
12	246	27.8	830	12	BC172019
13	155.4	18.3	686	10	BM551556
14	154.4	18.3	260	9	AA117088
15	154.4	18.3	888	14	BQ747434
16	144.6	13.5	679	18	BM571648
17	113	18.3	619	9	AL676863
18	111.4	13.1	693	13	BQ043488
19	111.4	13.1	914	14	BQ724151
20	109.8	12.9	916	14	BQ721562
21	69.6	8.2	491	17	AQ666525
22	66.2	7.5	660	13	BM488658
23	61.2	6.7	678	14	BM491724
24	60.8	6.5	614	13	BM439761
25	64.8	6.5	663	13	BM488497
26	51	6.0	629	13	B1067476
27	46.4	5.3	916	12	BQ757771
28	45	5.3	581	12	BE741425
29	44.6	5.1	468	12	BE715563
30	44.2	5.1	646	14	BQ745202
31	44.2	5.1	693	10	BM620731
32	44.2	5.1	909	14	BQ956841
33	44	5.1	425	10	BM530608
34	44	5.1	1303	9	AB090697
35	41.6	4.9	522	12	BF450618
36	41.6	4.9	759	13	BE152204
37	41.4	4.9	663	14	BQ138751
38	41.2	4.9	600	10	AB200140
39	41	4.8	871	17	CNS036AY
40	40.6	4.8	459	10	BE653429
41	40.6	4.8	489	10	BE478885
42	40.6	4.8	492	12	BE231059
43	40.6	4.8	507	10	BE476309
44	40.6	4.8	512	10	BE481963
45	40.6	4.8	532	10	BE588845

ALIGNMENTS

BM981657/c	BM981657	751 bp	gRNA	linear	EST 21 MAR-2002
DEFINITION	U1-CP-EN1-adi m-02-0-01-01-01-CP-EN1 Homo sapiens cDNA clone				
ACCESSION	BM981657				
VERSION	BM981657.1				
KEYWORDS	EST,				
SOURCE	human,				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 751)				
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery				
JOURNAL	Genome Res. 6 (9): 791-806 (1996)				
MEDLINE	97044477				
COMMENT	Submitted by Dr. M. H. Reuter, University of Iowa				

Submitted by Dr. M. H. Reuter, University of Iowa
McGraw Lab
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
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Fax: 319 336 7171
Email: paul.mccray@uiowa.edu
Library Preparation: Dr. M. H. Reuter, University of Iowa
cDNA Library Preparation: Dr. M. H. Reuter, University of Iowa
cDNA Library Arranged by: Dr. M. H. Reuter, University of Iowa
ARR & packed by: Dr. M. H. Reuter, University of Iowa

SELLER'S HOUSE MUST BE

$$H^1(K_{\mathbb{A}_f}, \mathcal{O}_f) = 0; \quad M_{\mathbb{A}_f}$$

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Search completed: December 12, 2002, 17:43:48
Job time : 2219 secs

